

SSPI

6358 TCATCAAAATATTTACGAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATC  
6417 AGTACGTTTAAATACTCTCGTAAGGTC TAACCCAAGTTAGTTGTTCCATGCTCGGTATAG  
6418 ACTTTATTTCAAAATTTGGTATCGCCAAAACCAAGAGAAGCACTCCCATCTCAAGGTTTGTA  
6477 TGAATAAAGTTTAAACCATPAGCGGTTTGGTTCTTCCCTTGAGGGTAGGAGTTTCCAAACAT  
6478 AGGAAGAAATTTCTCAGTCCAAGCCTCAACAAGGTCAGGCTACAGAGTCTCCAAACCATTA  
6537 TCTTTCTTAAGAGTCAAGTTTCCGAGTTGTTCCAGTCCCATGTCTCAGAGGTTTGTAAT  
6538 GCCAAAAGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAACACTACTGTTCAGCA  
6597 CCGTTTTCGATGTCCTTACGTTACTTCTTAGAAGTTAGTTTCAATTGATGACAAGGTCGT  
6598 CATGCAATCATGGTTCAGTTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAGTTAGTGG  
6657 GTACGTACGTACCAGTTCAATCAAGATCTTTTCTGTAGGTGGCTTCTGAATTTCAATCACC

Figure 1

SHEET 1 of 2

09137440 . 0820981699



559221 65049160

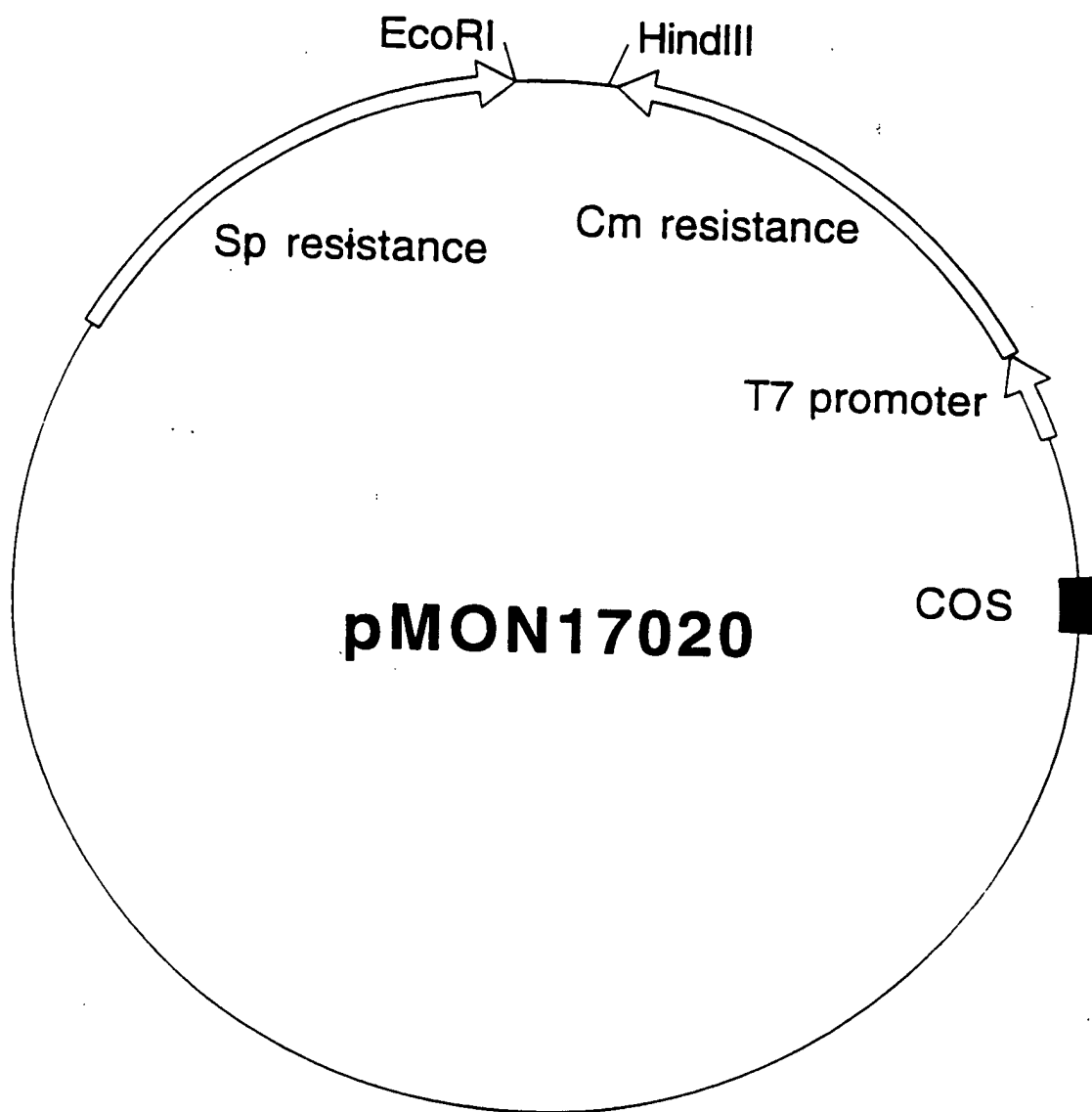


Figure 2



TTC GGC AAT GCC GCC ACC GGC TGC CGC CTG ACC ATG GGC CTC GTC GGC	394
Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly	
100	105
110	
GTC TAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG	442
Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys	
115	120
125	
CGC CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG	490
Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln	
130	135
140	
GTG AAA TCG GAA GAC GGT GAC CGT CTT CCC GTT ACC TTG CGC GGC CCG	538
Val Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro	
145	150
155	
AAG ACG CCG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG	586
Lys Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln	
160	165
170	175
GTG AAG TCC GCC•GTG CTG CTC GCC GGC CTC AAC ACG CCC GGC ATC ACG	634
Val Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr	
180	185
190	
ACG GTC ATC GAG CCG ATC ATG ACG CGC GAT CAT ACG GAA AAG ATG CTG	682
Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu	
195	200
205	

# Figure 3

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004454099-1124599



CGC	CGC	CCT	TCG	ATG	ATC	GAC	GAA	TAT	CCG	ATT	CTC	GCT	GTC	GCC	GCC	1066
Arg	Ala	Pro	Ser	Met	Ile	Asp	Glu	Tyr	Pro	Ile	Leu	Ala	Val	Ala	Ala	
320					325					330					335	

GCC	TTT	CGG	GAA	GGG	GCG	ACC	GTG	ATG	AAC	GGT	CTG	GAA	GAA	CTC	CGC	1114
Ala	Phe	Ala	Glu	Gly	Ala	Thr	Val	Met	Asn	Gly	Leu	Glu	Glu	Leu	Arg	
			340						345					350		

GTC	AAG	GAA	AGC	GAC	UGC	CTC	TCG	GCC	GTC	GCC	AAT	GGC	CTC	AAG	CTC	1162
Val	Lys	Glu	Ser	Asp	Arg	Leu	Ser	Ala	Val	Ala	Asn	Gly	Leu	Lys	Leu	
			355					360					365			

AAI	GGC	GTG	GAT	TGC	GAT	GAG	GGC	GAG	ACG	TCG	CTC	GTC	GTG	CGC	GGC	1210
Asn	Gly	Val	Asp	Cys	Asp	Glu	Gly	Glu	Thr	Ser	Leu	Val	Val	Arg	Gly	
		370					375					380				

CGC	CTT	GAC	GGC	AAG	UGG	CTC	GGC	AAC	GCC	TCG	GGC	GCC	GCC	GTC	GCC	1258
Arg	Pro	Asp	Gly	Lys	Gly	Leu	Gly	Asn	Ala	Ser	Gly	Ala	Ala	Val	Ala	
385						390					395					

ACC	CAT	CYC	GAT	CAC	CCC	AIC	GCC	ATG	AGC	TTC	CYC	GTC	ATG	GGC	CYC	1306
Thr	His	Ieu	Asp	His	Arg	Ile	Ala	Met	Ser	Phe	Ieu	Val	Met	Gly	Ieu	
400					405					410					415	

GTC	TTC	GAA	AAC	CCT	GTC	ACG	GTG	GAC	GAT	GCC	ACG	ATG	ATC	GCC	ACG	1354
Val	Ser	Glu	Asn	Pro	Val	Thr	Val	Asp	Asp	Ala	Thr	Met	Ile	Ala	Thr	
				420					425					430		

## Figure 3

ACC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCC AAG ATC	1402
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile	
435	
440	
445	
GAA CTC TCC GAT ACC AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGTC	1456
Glu Leu Ser Asp Thr Lys Ala Ala	
450	
455	
CCGCTTCGGG CCGCAAGGG AGCTCTCGC GCCGTATCGC GGAGTCTAT GCTTTCATC	1516
ATCTTCGATTAC GGGCCCTGACC TATCGGCCCA CGGCCAAAGC GCTGCTCGAT CGCGCCCTGT	1576
CGCTTCGATGA CGAGCGCGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG	1636
ACCGGTCGGT GCTGTGGGCC CATGCCATCG CGGAGCGGC TTCGAAGATC GCCGTCATGC	1696
CTTCGGTCCG GCGGGCGCTG GTCGAGCGGC AGCGCAGCTT TCGGGCGCGT GAGCCGGCA	1756
CGGTTCCTGGA TCGACGCCAT ATCGGCACGG TGGTCTGCCG GGATGCGCCG GTGAAGCTCT	1816
ATGTCACCGC GTCACCGGAA GTGCGCGGA AACGCCGCTA TGACGAATC CTCGGCAATG	1876
GCGGCTTCGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGACA	1936
TGGGTCGGGC GGACAGTCTT TCGAAGCCCG CCGACGATGC GCACTT	1982

# Figure 3

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CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG CTC	400
Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu	90
ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT ATC GGC	448
Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly	110
GAC GCC TCC CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC CCG TTG	496
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu	125
CCC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC ATG CCG	544
Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro	140
CTG ACC CTG ATC GGC CCG AAG ACC GCC AAT CCG ATC ACC TAT CGC GTG	592
Ileu Thr Ieu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr Arg Val	155
CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC GGT CTC	640
Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly Leu	170
AAC ACC CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC CGC GAC	688
Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr Arg Asp	190

# Figure 4

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09464099 121199

CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG 736  
 His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu 210  
 205 215

ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG 784  
 Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys 225  
 220 230

CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC 832  
 Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala 240  
 235 245

TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC 880  
 Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val Thr Ile 255  
 250 260 265

GGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG 928  
 Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu 270  
 275 280

CAG GAA ATG GGC GAT ATC GAA GTG CTC AAT GCC CGT CTT GCA GGC 976  
 Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly 285  
 290 295

GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC 1024  
 Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly 300  
 305 310

# Figure 4

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109464099 121599



ATC GCC ACC TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC	1408
Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly	
430	435
	440

GCA AAG ATC GAG TTT AGC ATG CTC TAGTCAC TCG ACAGCGAAA TATTTATTGC	1462
Ala Lys Ile Glu Leu Ser Ile Leu	
445	

GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGTTT AATGTCCAAT CTTCATACG	1522
---	------

TACACGACATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCG	1582
---	------

CTAAGCTTTC TCAAGACTTC GTTAAAACTG TACTGAATC CCGGGGGTC CGGGATCAA	1642
--	------

ATGACTTTCAT TTTCTGAGAAA TTGGCCTCGC A	1673
--------------------------------------	------

GTTGATTCGGCC CAAATATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG 54  
 Met Ser His Ser Ala Ser Pro 1 5

AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC 102  
 Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg 10 15 20

ATTT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT 150  
 Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly 25 30 35

CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC 198  
 Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp 40 45 50 55

GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT 246  
 Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg 60 65 70

AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG 294  
 Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu 75 80 85

TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG 342  
 Leu Glu Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala 90 95 100

**Figure 5** SHEET 1 of 5



GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG	726
Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln	
220	225
230	
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG	774
Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser	
235	240
245	
ACC GCC TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC	822
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val	
250	255
260	
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC	870
Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu	
265	270
275	
ACC TTG CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT	918
Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu	
280	285
290	
295	
GCA GGC GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC	966
Ala Gly Gly Glu* Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu	
300	305
310	
AAG GGC GTC GTC GTT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA	1014
Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu	
315	320
325	

## Figure 5

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004454000-1211544



TTT CCG GTC CTG GCG ATT GCC GCC TCC TTC GCG GAA GGC GAA ACC GTG 1062  
 Tyr Pro Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val 330 335 340

ATG GAC GGG CTC GAC GAA CTG CCG GTC AAG GAA TCG GAT CGT CTG GCA 1110  
 Met Asp Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala 345 350 355

GCG GTC GCA CGC GCG CTT GAA GCC AAC GCG GTC GAT TGC ACC GAA GGC 1158  
 Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly 360 365 370 375

GAG ATG TCG CTG ACG GTT CCG GCG CCG GAC GCG AAG GGA CTG GGC 1206  
 Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly 380 385 390

GGC GCG ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC 1254  
 Gly Gly Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe 395 400 405

CTC GTC ATG GCG CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT 1302  
 Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser 410 415 420

AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA 1350  
 Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly 425 430 435

# Figure 5

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00464099-121099

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAA 1400  
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu  
440 445

TATTAATTTGC GAGATTGGGC ATTATPACCG GTTGTCTCA GCGGGGTTT AATGTCCAAT 1460  
TTCCTACG TAACACGATC AGGAATATC AAAAAAGCTT 1500

## Figure 5

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09464099-121699







301 VADLRVRSSYLKGVTPVEDRAPSMIDEXPIILAVAAAFAGATVMNGLEEL 350  
|||||.|.|||||.||.:|||||:|:|.|.|.|||.|||:|:|  
301 VADLRVRASKIKGVVPPERAPSMIDEXPLAIAASFAGETVMDGLDEL 350  
351 RVKESIDRLSAVANGLKINGVDCDEGETSLVVRGRPDGKGLNASGAAVAT 400  
|||||.|||.|||.|||||.|||.||||| 1:|.|||  
351 RVKESDRLAAVARGLEANGVDCTEGEMSLTVRGRPDGKGLG..GGTVAT 397  
401 HLDHRIAMSEFLVMGLVSENPVTVDDATMIATSEFLFMDLMAGLAKIELS 450  
|||||.|||||.|||.|||||.|||||.|||:|:|  
398 HLDHRIAMSEFLVMGLAAEKPVTVDDSNMIATSEFLFMDMPGLGAKIELS 447  
451 LTRKAA\* 456  
448 LL.... 449

Figure 7

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09464009-124599

CCATGGCTTCA CGGTGCAAGC AGCCGTCACG CAACTGCTCG TAACTCCTCT GGTCTTTCTG	60
GAACCGTCCG TATTCCAGGT GACAAGTCTA TCTCCACAG GTCCCTTCATG TTTGGAGGTC	120
TGCGTACCGG TGAACCTCCG ATCACCGGTC TTTTGAAGG TGAAGATGTT ATCAACACTG	180
GTAAAGGCTAT GCAAGCTATT GGTCCAGAA TCCGTAAGGA AGGTGATACT TGGATCATTC	240
ATTGTTGTGG TTAACGGTGGG CTCTTGCTC CTGAGGCTCC TCTCGATTTC GGTAAACGCTG	300
CAACTGGTTG CCGTTTGACT ATGGGTCCTG TTGGTGTTTA CGATTTCGAT AGCACTTTCA	360
TTCGTGACCG TTCTCTCACP AAGCGTCCA TGGGTCGTGT GTTGAACCA CTTCGCGAAA	420
TGCGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGAGCCAA	480
AGACTTCCAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG	540
TTCCTGCTTG TGGTCTCAAC ACCCCAGGTA TCACCACCTGT TATCGAGCCA ATCATGACTC	600
GTGACCTACAC TGAAAAGATT CTTCAGAGGTT TTGGTGCTTA CCTTACCCTT GAGACTGATG	660
CTTGACCGTTG GCGTACCATT CGTCTTGAGG GTCGTGGTAA GCTCACCGGT CAAGTGATTG	720
ATTGTTCAGG TGATPCCATT TCTACTGCTT TCCCATTTGG TGCTGCCCTTG CTGTTPCCAG	780
GTTCGGACGT CACCATCCCT AACGTTTGA TGAACCCAAC CCGTACTGGT CTCATCTTGA	840

# Figure 8

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09464099-121649

CTCTGCAGGA AATGGGTGTC GACATCGAAG TGATCAACCC	ACGTCCTGCT	GGTGAGAAG	900
ACGTGCCCTGA CTTCGGGTGT CGTTCCTCTA CTTTGAAGG	TGTTACTGTT	CCAGAAGACC	960
GTTCCTCCCTTC TATGATCGAC GAGTATCCAA TTCTCGCTGT	TGCAGCTGCA	TTCCGCTGAAG	1020
GTTCCTAACCGT TATGAACCGGT TTGGAAGAAC TCCGTGTTAA	GGAAGCGAC	CGTCTTTCTG	1080
CTGTCCGCAAA CGGTCTCAAG CTCACGGTG TTGATTGCCA	TGAAGGTGAG	ACTTCTCTCG	1140
TTCGTGCCGTGG TCGTCCCTGAC GGTAAAGGTC TCGGTAACGC	TTCTGGAGCA	GCTGTGCTA	1200
CCCACCTTGA TCACCGTATTC GCTATGAGCT TCCTCGTTAT	GGGTCTCGTT	TCTGAAAACC	1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTACTAGCTT	CCCAGAGTTC	ATGGATTTGA	1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA	GGCTGCTTGA	TGAGCTC	1377

# Figure 8

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09464095.121099









AGA TCT TCT TCA AGA ATG GCA CAA ATT AAC AAC ATG GCT CAA GGG ATA CAA	49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln	
1	5
10	
ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT AAA TCT	97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser	
15	20
25	
TCA AGT TTT CTT GTT TTT GGA TCT AAA AAA CTG AAA AAT TCA GCA AAT	145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn	
30	35
40	
TCT ATG TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG TTT TGT	193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys	
45	50
55	
60	
TCC TTT AGG ATT TCA GCA TCA GTG GCT ACA GCC TGC ATG C	233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met	
65	70

Figure 11

AGATCTGCTA GAAATPAATTTT TGTTTAACTT TAAGAAGGAG ATATATCC ATG GCA CAA 57  
 Met Ala Gln 1

ATT AAC AAC ATG GCT CAA GGG ATA CAA ACC CTT AAT CCC AAT TCC AAT 105  
 Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn 5 10 15

TTC CAT AAA CCC CAA GTT CCT AAA TCT TCA AGT TTT CTT GTT TTT GGA 153  
 Phe His Lys Pro Gln Val Pro Lys Ser Ser Phe Leu Val Phe Gly 20 25 30 35

TCT AAA AAA CTG AAA AAT TCA GCA AAT TCT ATG TTG GTT TTG AAA AAA 201  
 Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys 40 45 50

09464000 124640

GAT TCA ATT TTT ATG CAA AAG TTT TGT TCC TTT AGG ATT TCA GCA TCA	249
Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser	
55	
60	
65	

GTT GCT ACA GCA CAG AAG CCT TCT GAG ATA GTG TTG CAA CCC ATT AAA	297
Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys	
70	
75	
80	

GAG ATT TCA GGC ACT GTT AAA TTG CCT GGC TCT AAA TCA TTA TCT AAT	345
Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn	
85	
90	
95	

AGA ATT C	352
Arg Ile	
100	

# Figure 12

SHEET 2 of 2

09464099-121699

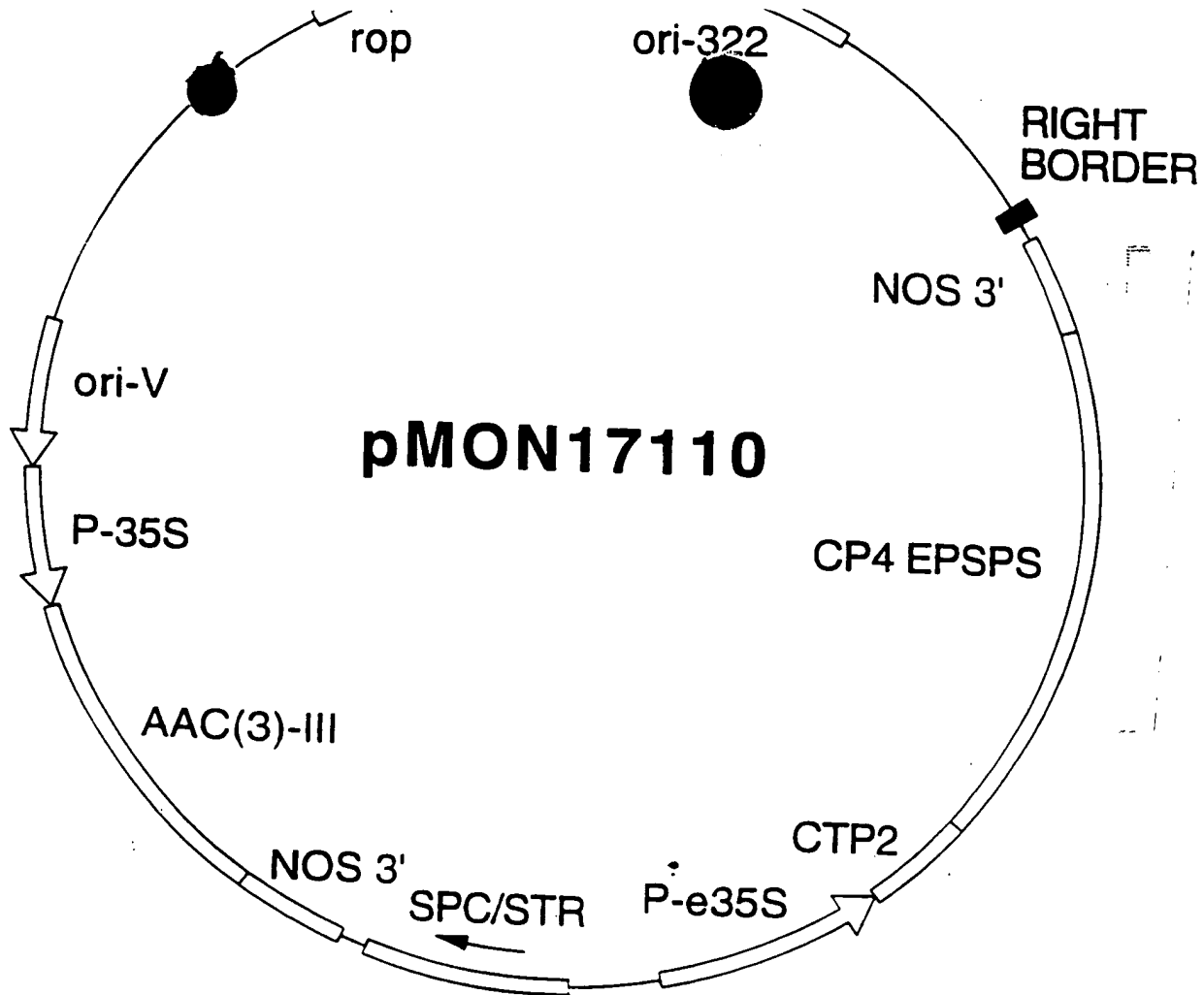


Figure 13

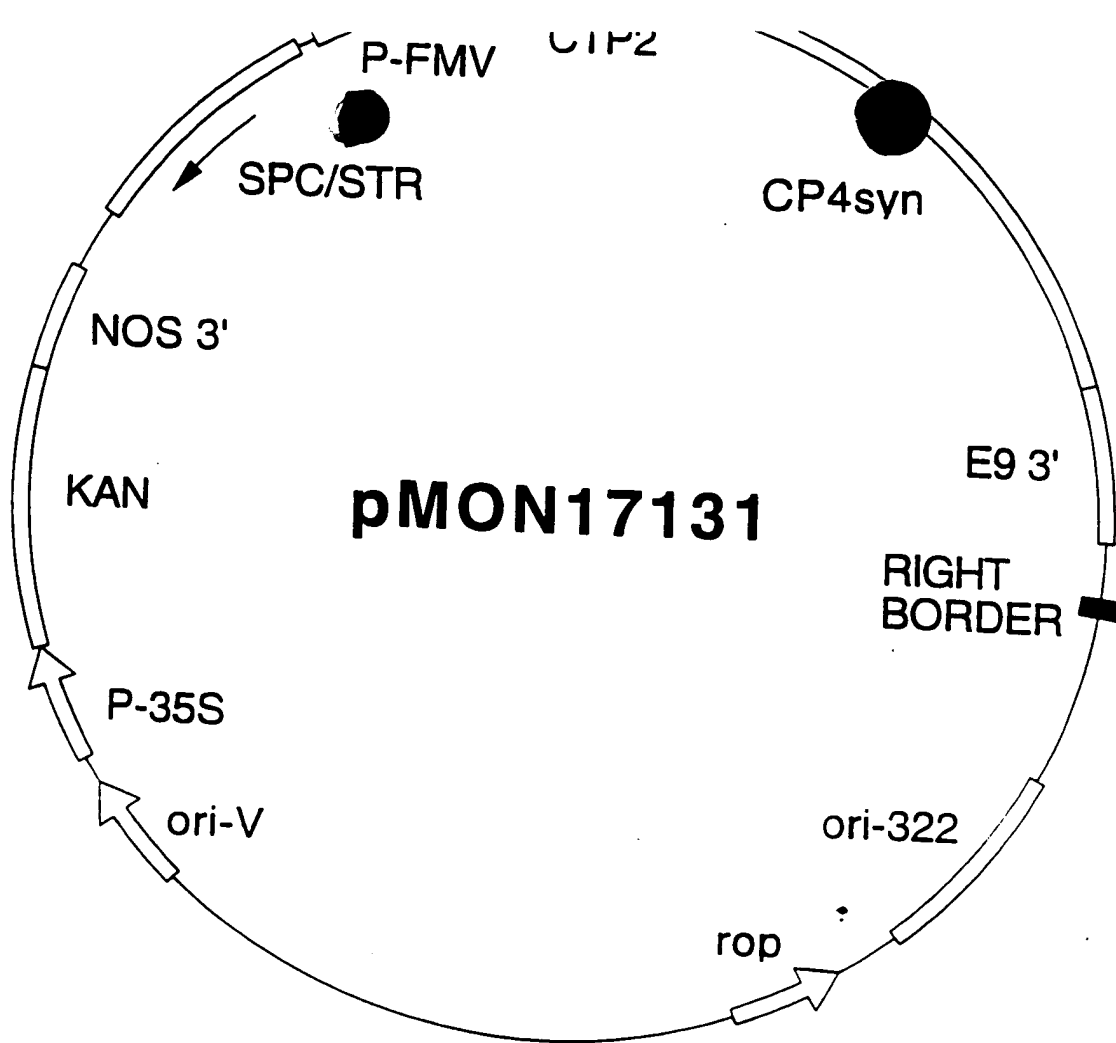


Figure 14

659727-65049460



6507960

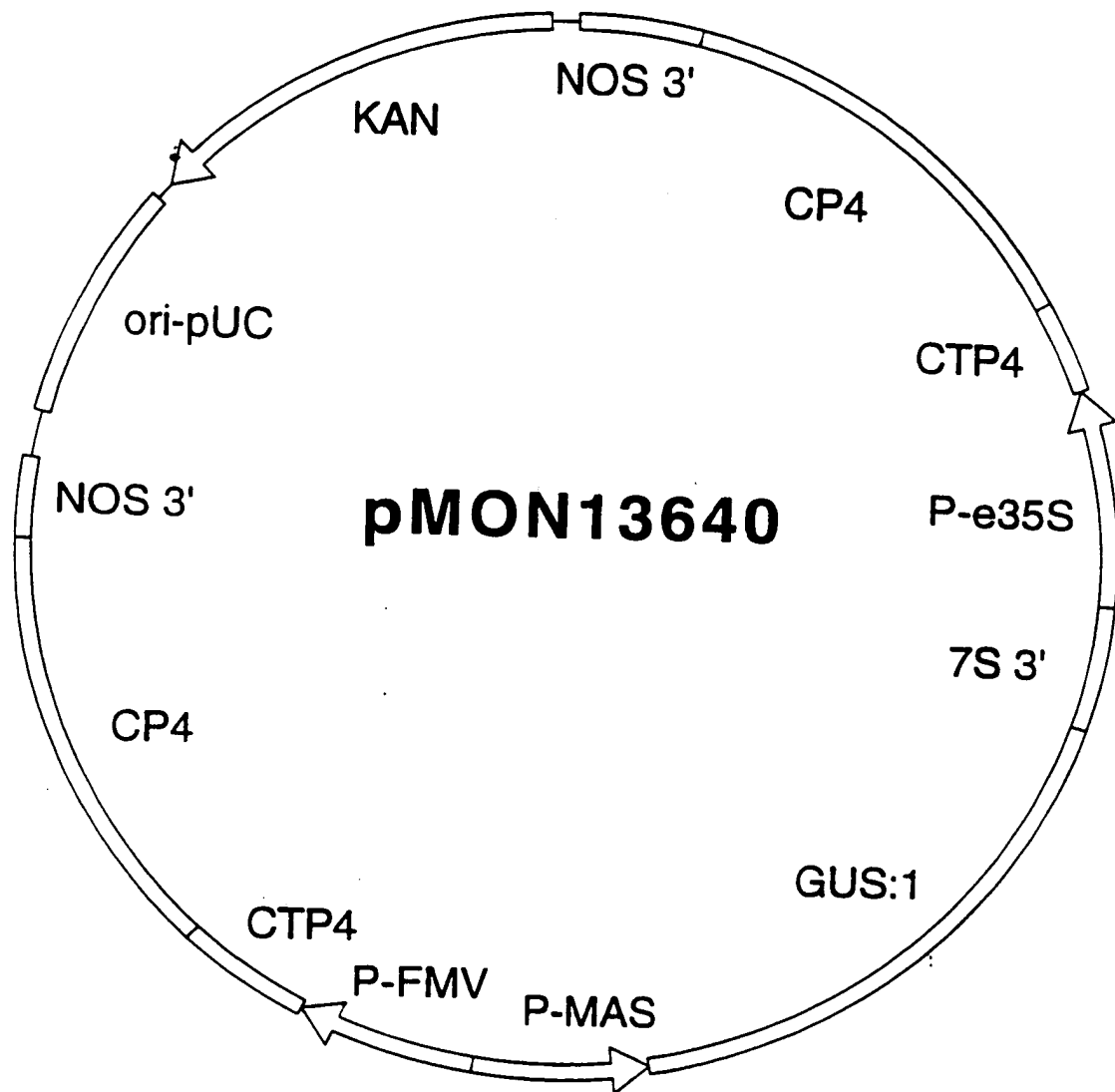


Figure 15

66949460

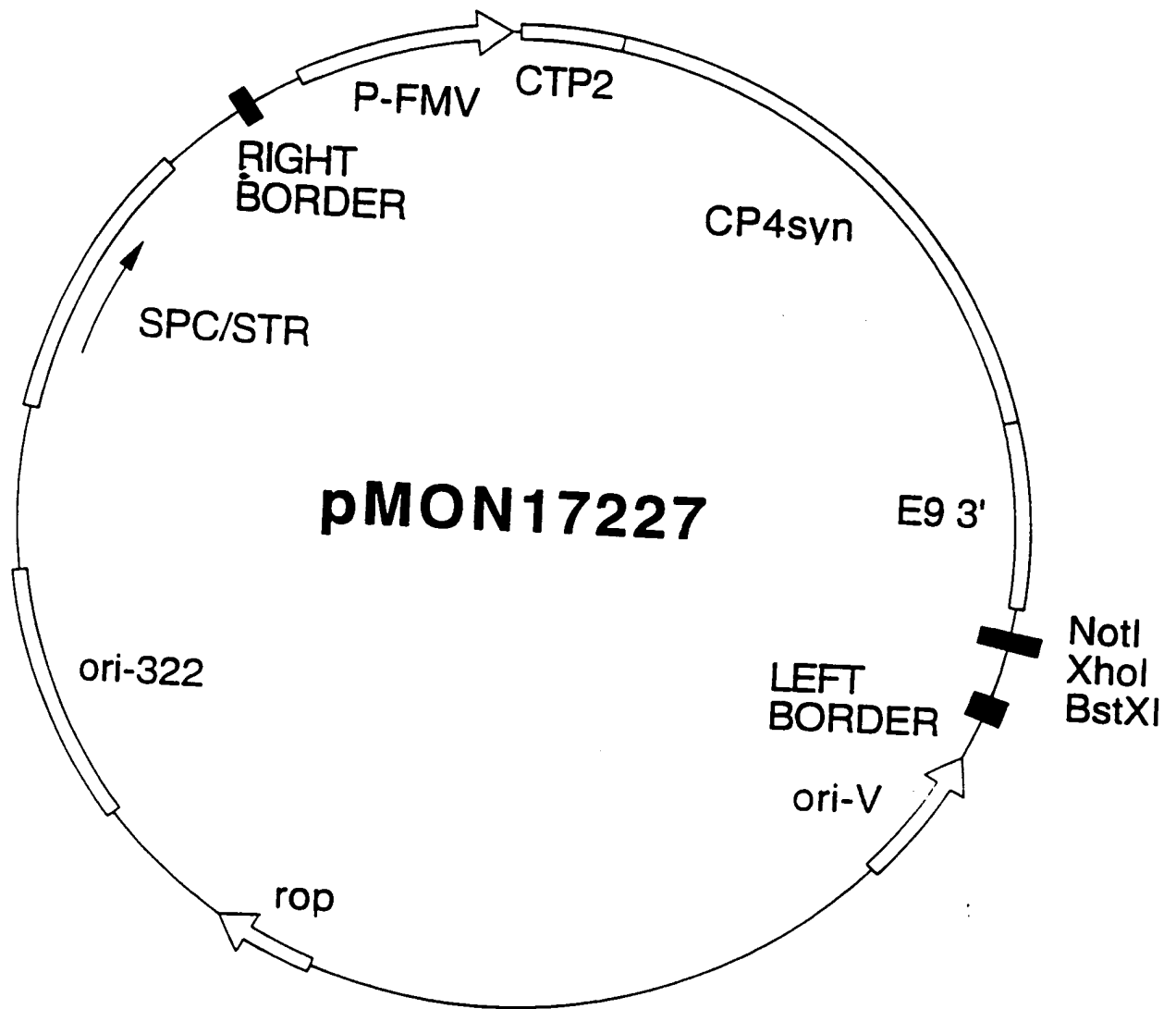


Figure 16

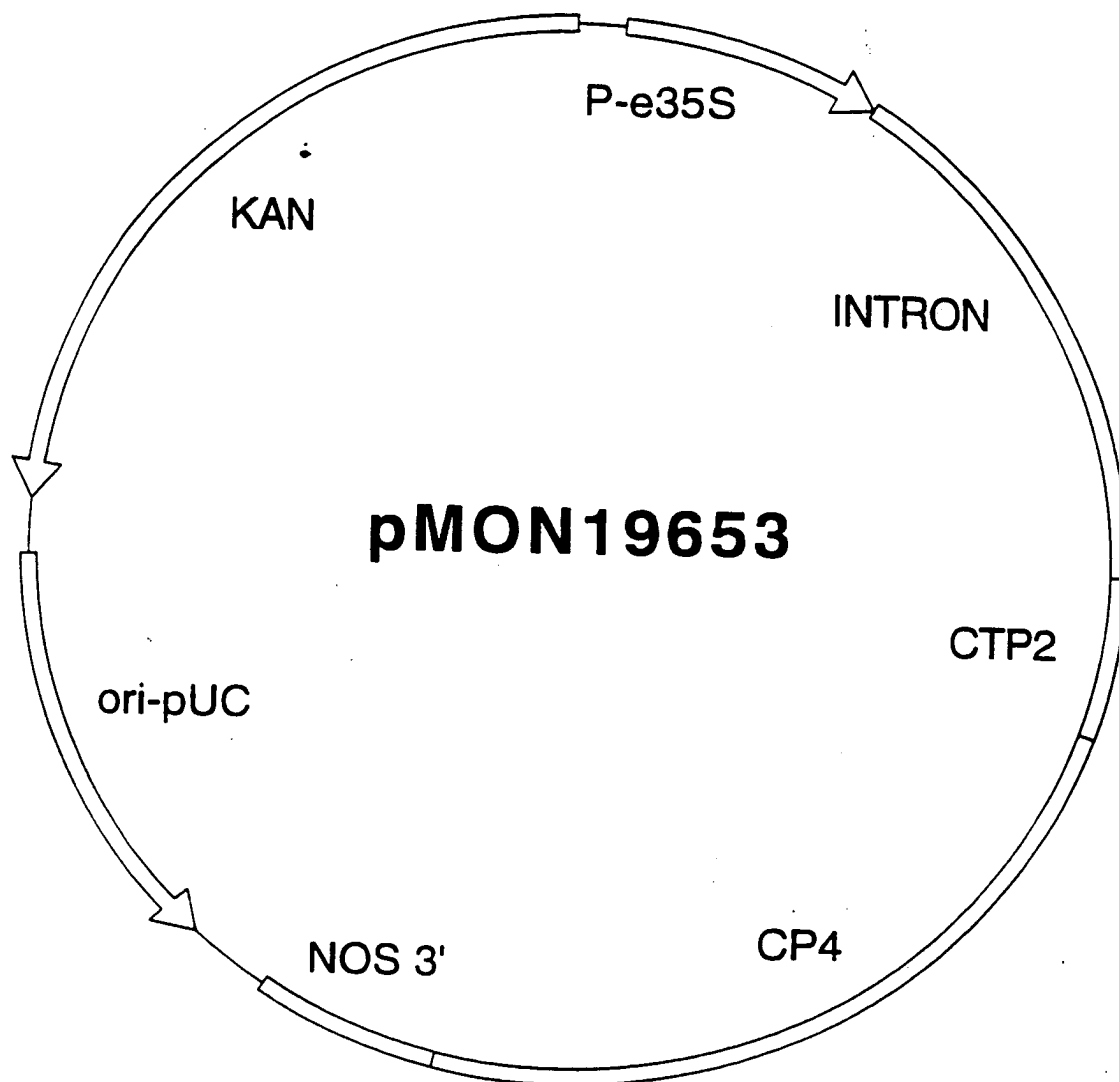


Figure 17

ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC	48
Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	
1 5 10 15	
GGT GAT AAA TCC ATG TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG	96
Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	
20 25 30	
GCA GGC ACA ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG	144
Ala Gly Thr Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	
35 40 45	
AGC ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC	192
Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser	
50 55 60	
AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG	240
Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu	
65 70 75 80	
CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG	288
Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu	
85 90 95	
ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA	336
Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	
100 105 110	

Figure 18

GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG	384
Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu	
115 120 125	
AAA AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGC GAG TTT ACA	432
Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Glu Phe Thr	
130 135 140	
CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA	480
Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser	
145 150 155 160	
CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA	528
Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu	
165 170 175	
CAG GCT GAG GGC ACA ACT GTA ACA GAG CCC CAT AAA TCT CGG GAC	576
Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp	
180 185 190	
CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT	624
His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp	
195 200 205	
CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT	672
Gln Thr Ser Val Ser Ile Ala Gly Gln Lys Leu Thr Ala Ala Asp	
210 215 220	

**SHEET 2 of 4**

ATT TTT GTT CCT GGA GAC ATT TCT TCA GCC GCG TTT TTC CTT GCT GCT	720
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala	235
225	240
GGC GCG ATG GTT CCA AAC AGC AGA ATT GTA TTG AAA AAC GTA GGT TTA	768
Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu	250
245	255
AAT CCG ACT CGG ACA GGT ATT ATT GAT GTC CTT CAA AAC ATG GGG GCA	816
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala	260
265	270
AAA CTT GAA ATC AAA CCA TCT GCT GAT AGC GGT GCA GAG CCT TAT GGA	864
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly	275
280	285
GAT TTG ATT ATA GAA ACG TCA TCT CTA AAG GCA GTT GAA ATC GGA GGA	912
Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly	290
295	300
GAT ATC ATT CCG CGT TTA ATT GAT GAG ATC CCT ATC ATC GCG CTT CTT	960
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu	305
310	315
GGC ACT CAG GCG GAA GGA ACC ACC GTT ATT AAG GAC GCG GCA GAG CTA	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	320
325	330
335	

Figure 18



ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GGC GAA	48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	
1 5 10 15	
ATA GAA GTG CCG GCC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG	96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	
20 25 30	
ACG TCG CTA GCT GAA GGT GTA TCT ACT ATA TAT AAG CCA CTA CTT GGC	144
Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly	
35 40 45	
GAA GAT TGT CGT CGT ACG ATG GAC ATT TTC CGA CAC TTA GGT GTA GAA	192
Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu	
50 55 60	
ATC AAA GAA GAT GAT GAA AAA TTA GTP GTG ACT TCC CCA GGA TAT CAA	240
Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln	
65 70 75 80	
GTP AAC ACG CCA CAT CAA GTA TTG TAT ACA GGT AAT TCT GGT ACG ACA	288
Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr	
85 90 95	
ACA CGA TTA TTG GCA GGT TTG TTA AGT GGT TTA GGT AAT GAA AGT GTP	336
Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val	
100 105 110	

Figure 19



TTTG TCTT GGC GAT GTTT TCCA ATTG GGT AAA AGG CCA ATG GAT CGT GTC TTG 384  
 Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu 115 120 125

AGA CCA TTG AAA CTT ATG GAT GCG AAT ATT GAA GGT ATT GAA GAT AAT 432  
 Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn 130 135 140

TAT ACC CCA TTG AATT AATT AAG CCA TCT GTC ATA AAA GGT ATA AAT TAT 480  
 Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr 145 150 155 160

CAA ATG GAA GTT GCA AGT GCA CAA GTA AAA AGT GCC ATT TTA TTT GCA 528  
 Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala 165 170 175

AGT TTG TTT TCT AAG GAA CCG ACC ATC ATT AAA GAA TTA GAT GTA AGT 576  
 Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser 180 185 190

CGA AAT CAT ACT GAG ACG ATG TTC AAA CAT TTT AAT ATT CCA ATT GAA 624  
 Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu 195 200 205

GCA GAA GCG TTA TCA AATT AAT ACA ACC CCT GAA GCA ATT ATT CGA TAC ATT 672  
 Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile 210 215 220

**Figure 19**

09464099-123699

AAA CTT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC 720  
 Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe 225 230 235 240

TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT 768  
 Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His 245 250 255

AAT GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA 816  
 Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu 260 265 270

AAA ATT GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA 864  
 Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu 275 280 285

CCT ACT GCT TCT ATT CCGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA 912  
 Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile 290 295 300

ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA 960  
 Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val 305 310 315 320

ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT 1008  
 Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp 325 330 335

Figure 19 SHEET 3 of 4

09464094.121549

GCG GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT 1056  
 Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala 340 345 350

GAT ATG TTA AAC TTG TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA 1104  
 Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly 355 360 365

TTG ATP ATP CAT CCG TCA GAA TTT AAA ACA AAT GCA ACA GAT ATT TTA 1152  
 Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu 370 375 380

ACT GAT CAT CGA ATA GGA ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA 1200  
 Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser 385 390 395 400

ACC GAG CCG GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT 1248  
 Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe 405 410 415

CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA 1293  
 Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly 420 425 430

# Figure 19

SHEET 4 of 4

09464039-124599

PG2982	.....	.....	MSHSASPKPA	TARRSEALTG	50
LBAA	.....	.....	MSHSASPKPA	TARRSEALTG	
Agrobacterium CP4	.....	.....	MSHSASPKPA	TARRSEALTG	
B. subtilis	.....	.....	MSHGASSRPA	TARKSSGLSG	
S. aureus	.....	.....	.....	M KRDKVQTLHG	
S. cerevisiae	.....	.....	.....	MVNEQ IIDISGPLKG	
A. nidulans	.....	.....	.....	LVYP FKDIPADQK	
B. napus	.....	.....	.....	VHP . GVAHSSNV	
A. thaliana	.....	.....	K...	ASEI VLQPIREISG	
N. tabacum	.....	.....	K...	ASEI VLQPIREISG	
L. esculentum	.....	.....	K...	PNEI VLQPIKDISG	
P. hybrida	.....	.....	K...	PHEI VLXPIKDISG	
Z. mays	.....	.....	K...	PSEI VLQPIKEISG	
S. gallinarum	.....	.....	AGAEI	VLQPIKEISG	
S. typhimurium	.....	.....	MESL	TLQPIARVDG	
S. typhi	.....	.....	MESL	TLQPIARVDG	
E. coli	.....	.....	MESL	TLQPIARVDG	
K. pneumoniae	.....	.....	MESL	TLQPIARVDG	
Y. enterocolitica	.....	.....	MESL	TLQPIARVDG	
H. influenzae	.....	.....	MESL	TLHPIALING	
P. multocida	.....	.....	MEKI	TLAPISAVEG	
A. salmonicida	.....	.....	MIKDATAI	TLNPISYIEG	
B. pertussis	.....	.....	NSL	RLEPISRVAE	
Consensus	.....	.....	MSGLAYL	DLPAARLARG	

Figure 20

PG2982	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK	100
LBAA	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK	
Agrobacterium CP4	TVRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	KAMQAM.GAR	
B. subtilis	EIHIPGDKSI	SHRSVMFGAL	AAGTTVKNF	LPGADCLSTI	DCFRLM.GVH	
S. aureus	EIEVPGDKSM	THRAIMLASL	AEGVSTIYKP	LLGEDCRRTM	DIFRHL.GVE	
S. cerevisiae	VVIPGSKSI	SNRALILAAL	GEGQCKIKNL	LHSDDTKHML	TAVHELKAT	
A. nidulans	ICAPPGSKSI	SNRALVLAAL	GSGTCRIKNL	LHSDDTEVML	NALERLGAAT	
B. napus	LIKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LNSDDINMYL	DALKKL.GLN	
A. thaliana	LIKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LNSDDINMYL	DALKRL.GLN	
N. tabacum	TVKLPGSKSL	SNRILLLAAL	SKGRTVVDNL	LSDDDIHYML	GALKTL.GLH	
L. esculentum	TVKLPGSKSL	SNRILLLAAL	SEGRTVVDNL	LSDDDIHYML	GALKTL.GLH	
P. hybrida	TVKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LSSDDIHYML	GALKTL.GLH	
Z. mays	TVKLPGSKSL	SNRILLLAAL	SEGTTVVDNL	LNSDDVHYML	GALRTL.GLS	
S. gallinarum	AINLPGSKSV	SNRALLLAAL	ACGKTVLTNL	LDSDDVRRHML	NALSAL.GIN	
S. typhimurium	AINLPGSKSV	SNRALLLAAL	PCGKTALTNL	LDSDDVRRHML	NALSAL.GIN	
S. typhi	AINLPGSKSV	SNRALLLAAL	ACGKTVLTNL	LDSDDVRRHML	NALSAL.GIN	
E. coli	TINLPGSKTV	SNRALLLAAL	AHGKTVLTNL	LDSDDVRRHML	NALTAL.GVS	
K. pneumoniae	TVNLPGSKSV	SNRALLLAAL	ARGTTVLTNL	LDSDDVRRHML	NALSAL.GVH	
Y. enterocolitica	TVNLPGSKSV	SNRALLLAAL	AEGTTQLNML	LDSDDIRHML	NALQAL.GVK	
H. influenzae	TINLPGSKSL	SNRALLLAAL	AKGTTKVTNL	LDSDDIRHML	NALKAL.GVR	
P. multocida	EVRLPGSKSL	SNRALLLAAL	AKGKTTLTNL	LDSDDVRRHML	NALKEL.GVT	
A. salmonicida	EVNLPGSKSV	SNRALLLAAL	ARGTTRLTNL	LDSDDIRHML	AALTQL.GVK	
B. pertussis	EVALPGSKSI	SNRVLLLAAL	AEGSTEITGL	LDSDDTRVML	AALRQL.GVS	
Consensus	PG-K--	R-----	L--G-----	L--D-----		

Figure 20

09464997-121599

	PG2982	101		150		
	LBAA	IRKEGDVWII	NGVNGCLLQ	I'.....EAA	LDFGNAGTGA	RLTMGLVGTY
Agrobacterium CP4		IRKEGDVWII	NGVNGCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY
B. subtilis		IRKEGDTWII	DGVNGGLLA	P.....EAP	LDFGNAATGC	RLTMGLGVY
S. aureus		IEQSSSDVVI	HKGIDALKE	P.....ESL	LDVNSGTTI	RLMLGILAGR
S. cerevisiae		IKEDDEKLIV	TSPGYQ.VNT	P.....HQV	LYTGNSTTT	RLLAGLLSGL
A. nidulans		ISWEDNGETV	VVEGHG...	..STLSACADP	LYLGNAGTAS	RFLTSLAALV
B. napus		FSWEEEGEVL	VVNGKG...	..NLQASSSP	LYLGNAGTAS	RFLTVAATLA
A. thaliana		VERDSVNNRA	VVEGCGGIFP	ASLDSKSDIE	LYLGNAGTAM	RPLTAAVTAA
N. tabacum		VETDSENNRA	VVEGCGGIFP	ASIDSKSDIE	LYLGNAGTAM	RPLTAAVTAA
L. esculentum		VEDDNEHQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAVTAA
P. hybrida		VEDDNEHQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAVTAA
Z. mays		VEEDSANQRA	VVEGCGGLFP	VGKESKEEIQ	LFLGNAGTAM	RPLTAAVTAA
S. gallinarum		VEADKAAKRA	VVVGCGGKFP	VE.DAKEEVQ	LFLGNAGTAM	RPLTAAVTAA
S. typhimurium		YTL.SADRTTC	DITGNGGPLR	AP.....GALE	LFLGNAGTAM	RPLAALCL.
S. typhi		YTL.SADRTTC	DITGNGGALR	AP.....GALE	LFLGNAGTAM	RPLAALCL.
E. coli		YTL.SADRTTC	DITGNGGPLR	AS.....GTLE	LFLGNAGTAM	RPLAALCL.
K. pneumoniae		YTL.SADRTTC	EIINGGPLH	AE.....GALE	LFLGNAGTAM	RPLAALCL.
Y. enterocolitica		YVLSSDRTRC	EVTGTGGLQ	AG.....SALE	LFLGNAGTAM	RPLAALCL.
H. influenzae		YRLSADRTTC	EVDGLGKLV	AE.....QPLE	LFLGNAGTAM	RPLAALCL.
P. multocida		YQLSDDKTIC	EIEGLGAFN	IQ.....DNLS	LFLGNAGTAM	RPLTAALCLK
A. salmonicida		YQLSEDKSVC	EIEGLGRAFE	WQ.....SGLA	LFLGNAGTAM	RPLTAALCLS
B. pertussis		YKLSADKTEC	TVHGLGRSFA	VS.....APVN	LFLGNAGTAM	RPLCAALCL.
Consensus		VGEVAD..GC	VTIEGVARFP	TE.....QAE	LFLGNAGTAF	RPLTAALALM
		-----	-----	-----	L--GN--T--	R-----

Figure 20

09464099-121699







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*Agrobacterium* CP4

VIEPVMTRDH	TEKMLQGFGA	DLTVETDKDG	VRHIRITGQG	KLVGQ.TIDV
VIEPVMTDRD	TEKMLQGFGA	DLTVEYDKDG	VRHIRITGQG	KLVGQ.TIDV
VIEPIIMTRDH	TEKMLQGFGA	NLTVEYTDADG	VRTIRLEGRG	KLTO.VIDV
VIEPHKSBDH	TEBMLQGFGA	NLTVEYTDADG	VRTIRLEGRG	KLTO.VIDV

VI EPVMT RDH	TEKMLQGF GA	DLTVETDKDG	VRHIRITGQG	KL VGQ. TIDV	300
VI EPVMT RDH	TEKMLQGF GA	DLTVETDKDG	VRHIRITGQG	KL VGQ. TIDV	
VI EPIMTRDH	TEKMLQGF GA	NLTVETDADG	VRTIRLEGRG	KL TGQ. VIDV	
VI EPHKSRDH	TERMLSAFGV	KLSEDQTS. .	VS IAGGQ	KLTA. DIFV	
IKELDVSRNH	TEEMERUDAT				

VIEPVMTRDH	TEKMLQGFCA	DLTVETDKDG	VRHIRITGQ	KLVGQ.TIDV	300
VIEPVMTRDH	TEKMLQFGA	DLTVETDKDG	VRHIRITGQ	KLVGQ.TIDV	
VIEPIMTRDH	TEKMLQFGA	NLTVETDADG	VRTIRLEGRG	KL TGQ.VIDV	
VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGQ	KLTA.DIFV	
IKELDVSRNH	<u>TE</u> TMFKHFN	PIEAGLS..	..INTPEAI	RYIKPADFHV	
GKPI SKIYVD	<u>MT</u> TVAGVTC				

[illegible][illegible][illegible][illegible]

3000	VIEPVMTRDH	TEKMLQGFCA	DLTIVETDKDG	VRHIRITGQG	KLVGQ.TIDV
	VIEPVMTRDH	TEKMLQGFCA	DLTVETDKDG	VRHIRITGQG	KLVGQ.TIDV
	VIEPIMTRDH	TEKMLQGFCA	NLTVETDADG	VRTIRLEGRG	KL TGQ.VIDV
	VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGGQ	KLTA.A.DIFV
	IKELDVSRNH	TETMFKHFN	PIEAGLS..	..INTPEAI	RYIKPADFHV
	GKPI SKLYD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI
	GKPI SQPYD	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNP AEYVI
	DKLISVPYVE	MTLKLMEKFG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEKFG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEKFG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV

VIEPVMTRDH	TEKMLÖFGA	DLTIVETDKDG	VRHIRITGÖG	KLVGÖ.TIDV	300
VIEPVMTRDH	TEKMLÖFGA	DLTIVETDKDG	VRHIRITGÖG	KLVGÖ.TIDV	
VIEPIMTRDH	TEKMLÖFGA	NLTIVETDADG	VRTIRLEGRG	KLTGÖ.VIDV	
VIEPHKSRDH	TERMLSAFGV	KLSEDÖTS..	...VSIAGGÖ	KLTA.A.DIFV	
IKELDVSRNH	<u>TE</u> TMFKHFN	PIEAEGLS..	..INTPREAI	RYIKPADFHV	
GKPISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
GKPISQPYID	MTTAMMRSFG	ID..VÖKSTT	EEHTYHIPÖG	RYVNPAEYVI	
DKLISVPYVE	MTLKLMEKFG	VS..AEHSDS	WDRFFVKGGÖ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEKFG	VS..VEHSDS	WDRFFVKGGÖ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEKFG	VS..VEHTSS	WDKFLVRGGÖ	KYKSPGKAYV	
DKLISVPYVE	MTLKLMEKFG	VF..VEHSSG	WDRFLVRGGÖ	KYKSPGKAYV	

VIEPVMTRDH	TEKMLQGFCA	DI'IVETDKDG	VRHIRITGQ	KLVGQ.TIDV	3000
VIEPVMTRDH	TEKMLQGFCA	DI'IVETDKDG	VRHIRITGQ	KLVGQ.TIDV	
VIEPIMTRDH	TEKMLQGFCA	NLTVEITDADG	VRTIRLEGRG	KL TGQ.VIDV	
VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGQ	KLTA.A.DIFV	
IKELDVSRNH	<u>TE</u> TMFKHFNI	PIEAEGLS..	..INTPEAI	RYIKPADFHV	
GKPI SKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
GKPI SQPYID	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNP AEYVI	
DKLISVPYVE	MTLKLMEFRG	VS..AEHSDS	WDRFFVKGQ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEFRG	VS..VEHSDS	WDRFFVKGQ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEFRG	VS..VEHTSS	WDKFLVRGQ	KYKSPGKAYV	
DKLISVPYVE	MTLKLMEFRG	VF..VEHSSG	WDRFLVKGQ	KYKSPGKAFV	
DKLISVPYVE	MTLKLMEFRG	IS..VEHSSS	WDRFFVVRGQ	KYKSPGKAEV	

VIEPVMTRDH	TEKMLÖFGA	DLTVETDKDG	VRHIRITGÖG	KLVGÖ.TIDV	3000
VIEPVMTRDH	TEKMLÖFGA	DLTVETDKDG	VRHIRITGÖG	KLVGÖ.TIDV	
VIEPIMTRDH	TEKMLÖFGA	NLTVEVDADG	VRTIRLEGRG	KLTGÖ.VIDV	
VIEPHKSRDH	TERMLSAFGV	KLSEDÖTS..	..VSIAGGÖ	KLTA.A.DIFV	
IKELDVSRNH	TETMEKHFNI	PIEAEGLS..	..INTPEAI	RYIKPADFHV	
GKPIISKLYVD	MTIKMMEKEFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
GKPISQPYID	MTTAMMRSGF	ID..VÖKSTT	EEHTYHIPÖG	RYVNPAEYVI	
DKLISVPYVE	MTLKLMEFRG	VS..AEHSDS	WDRFFVKGGÖ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEFRG	VS..AEHSDS	WDRFFVKGGÖ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEFRG	VS..VEHSDS	WDRFFVKGGÖ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEFRG	VS..VEHTSS	WDKFLVRGGÖ	KYKSPGKAYV	
DKLISVPYVE	MTLKLMEFRG	VF..VEHSSG	WDRFLVKGGÖ	KYKSPGKAFV	
DKLISVPYVE	MTLKLMEFRG	IS..VEHSSS	WDRFFVVRGGÖ	KYKSPGKAFV	
DKLISIPYVE	MTLRLMERFG	VK..AEHSDS	WDRFYIKGGÖ	KYKSPKNAV	
ELVSKPYVD	TTMLMERFG				

VIEPVMTRDH	TEKMLQGFCA	DLTVETDKDG	VRHIRITGQG	KLVGQ.TIDV
VIEPVMTRDH	TEKMLOGFGA	DLTVEETDKDG	VRHIRITGQG	KLVGQ.TIDV
VIEPIMTRDH	TEKMLQGFCA	NLTVEETDADG	VRTIRLEGRG	KL TGQ.VIDV
VTEPHKS RDH	TERMLS AFV	KLSEDO TS..	.. VSIAGGQ	KLTA.A.DIFV
IKELDVSRNH	TETMFKH FNI	PIEAEGLS..	..INTPEAI	RYIKPADFHV
GKPISKLYVD	MTIKMEKEFG	IN.VET.STT	EPTYTYIPKG	HYINPSEYVI
GKPISQPYID	MTTAMRSFG	ID..VO KSTT	EEHTYHIPQG	RYVNPAEYVI
DKLISVPYE	MTLKLMEFRG	VS..AEHS DS	WDRFFVKGGQ	KYKSPGNAYV
DKLISVPYE	MTLKLMEFRG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV
DKLISVPYE	MTLKLMEFRG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV
DKLISVPYE	MTLKLMEFRG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKA FV
DKLISVPYE	MTLKLMEFRG	IS..VEHSSS	WDRFFVRGGQ	KYKSPGKA FV
DKLISIPYE	MTLRIMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV
JELVLSKPYID	ITLNLMKT FG	VE..IAN.HH	YOQFVVKGGQ	OYHSBGRYIV
FELVSKPDVD	ITLNLMKT FG	VE..IAN.HH	YOQFVVKGGQ	OYHSBGRYIV

3000	VI E P V M T R D H	TE K M L Ö G F G A	D L T V E T D K D G	V R H I R I T G Ö G	K L V G Ö . T I D V
	VI E P V M T R D H	TE K M L Ö G F G A	D L T V E T D K D G	V R H I R I T G Ö G	K L V G Ö . T I D V
	VI E P I M T R D H	TE K M L Ö G F G A	N L T V E T D A D G	V R T I R L E G R G	K L T G Ö . V I D V
	V I E P H K S R D H	TE R M L S A F G V	K L S E D Ö T S . .	. . . V S I A G G Ö	K L T A A . D I F V
	I K E L D V S R N H	T E T M F K H F N I	P I E A E G L S . .	. . I N T P E A I	R Y I K P A D F H V
	G K P I S K L Y V D	M T I K M M E K F G	I N . V E T . S T T	E P Y T Y Y I P K G	H Y I N P S E Y V I
	G K P I S Ö P Y I D	M T T A M M R S F G	I D . V Ö K S T T	E E H T Y H I P Ö G	R Y V N P A E Y V I
	D K L I S V P Y V E	M T L K L M E R F G	V S . . A E H S D S	W D R F F V K G G Ö	K Y K S P G N A Y V
	D K L I S V P Y V E	M T L K L M E R F G	V S . . V E H S D S	W D R F F V K G G Ö	K Y K S P G N A Y V
	D K L I S V P Y V E	M T L K L M E R F G	V S . . V E H T S S	W D K F L V R G G Ö	K Y K S P G K A Y V
	D K L I S V P Y V E	M T L K L M E R F G	V F . . V E H S S G	W D R F L V K G G Ö	K Y K S P G K A F V
	D K L I S V P Y V E	M T L K L M E R F G	I S . . V E H S S S	W D R F F V R G G Ö	K Y K S P G K A F V
	D K L I S I P Y V E	M T L R L M E R F G	V K . . A E H S D S	W D R F Y I K G G Ö	K Y K S P K N A Y V
	D E L V S K P Y I D	I T L N L M K T F G	V E . . I A N . H H	Y Ö Ö F V V K G G Ö	Ö Y H S P G R Y L V
	D E L V S K P Y I D	I T L N L M K T F G	V E . . I A N . H H	Y Ö Ö F V V K G G Ö	Ö Y H S P G R Y L V
	E I V S K P Y I D	I T L N L M K T F G	V E . . I A N . H H	Y Ö Ö F V V K G G Ö	Ö Y H S P G R Y L V

[illegible]

3000	VIEPVMTRDH	TEKMLQGFCA	DLTIVETDKDG	VRHIRITGQG	KLVGQ.TIDV
	VIEPVMTRDH	TEKMLQGFCA	DLTIVETDKDG	VRHIRITGQG	KLVGQ.TIDV
	VIEPIMTRDH	TEKMLQGFCA	NLTIVETDADG	VRTIRLEGRG	KL TGQ.VIDV
	VIEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGGQ	KLTA.DIFV
	IKELDVSRNH	TEMTFKHFNI	PIEAGLS..	..INTPEAI	RYIKPADFHV
	GKPI SKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI
	GKPI SQPYID	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNPAYEYVI
	DKLISVPYVE	MTLKLMEFRG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEFRG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEFRG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV
	DKLISVPYVE	MTLKLMEFRG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV
	DKLISVPYVE	MTLKLMEFRG	IS..VEHSSS	WDRFFVVRGGQ	KYKSPGKAFV
	DKLISIPYVE	MTLRLMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV
	DELVSKPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DLVSKPYID	ITLNLMTKTFG	VE..IEN.QH	YQQFVVKGGQ	SYOSPGTYIV

VIEPVMTRDH	TEKMLQGFCA	DI'IVETDKDG	VRHIRITGQ	KLVGQ	TIDV
VIEPVMTRDH	TEKMLQGFCA	DLTVEITDKDG	VRHIRITGQ	KLVGQ	TIDV
VIEPIMTRDH	TEKMLQGFCA	NLTVEITDADG	VRTIRLEGRG	KL TGQ	VIDV
VTEPHKSRDH	TERMLSAFGV	KLSEDQTS	...VSIAGQ	KLTA	DIFV
IKELDVSRNH	<u>TE</u> TMFKHFNI	PIEAEGLS	..INTPREAI	RYIKPADFHV	
GKPI SKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
GKPI SQPYID	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNPAEYVI	
DKLISVPYVE	MTLKLMEKFG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEKFG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV	
DKLISVPYVE	MTLKLMEKFG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV	
DKLISVPYVE	MTLKLMEKFG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV	
DKLISIPYVE	MTLKLMEKFG	IS..VEHSSS	WDRFFVRGGQ	KYKSPGKAFV	
DKLISIPYVE	MTLRLMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV	
BEELVSKPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV	
BEELVSKPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV	
BEELVSKPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV	
BEELVSKPYID	ITLNLMTKTFG	VE..IEN.QH	YQQFVVKGGQ	SYQSPGTYL	
BEELVSKPYID	ITLNLMTKTFG	VE..VEN.QA	YQRFIVRGNO	QYOSPCDVI	

	VIEPVMTRDH	TEKMLQGFCA	DLTVETDKDG	VRHIRITGQG	KLVGQ.TIDV	300
	VIEPVMTRDH	TEKMLOGFGA	DLTVEETDKD	VRHIRITGQG	KLVGQ.TIDV	
	VIEPIMTRDH	TEKMLQGFCA	NLTVEETDADG	VRTIRLEGRG	KL TGQ.VIDV	
	VTEPHKS RDH	TERMLSAGFV	KLSEDO TS..	.. VSIAGGQ	KL TAA.DIFV	
	IKELDVSRNH	TETMFKH FNI	PIEAEGLS..	.. INTPEAI	RYIKPADFHV	
	GKPISKLVD	MTIKMEKEFG	IN.VET.STT	EPTYTYIPKG	HYINPSEYVI	
	GKPISOPIYD	MTTAMMSFG	ID..VO KSTT	EEHTYHIPQG	RYNPAEYVI	
	DKLISVPYVE	M TLKLMERFG	VS..AEHS DS	WDRFFVKGGQ	KYKSPGNAYV	
	DKLISVPYVE	M TLKLMERFG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV	
	DKLISVPYVE	M TLKLMERFG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV	
	DKLISVPYVE	M TLKLMERFG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKA FV	
	DKLISVPYVE	M TLKLMERFG	IS..VEHSSS	WDRFFVRGGQ	KYKSPGKA FV	
	DKLISIPIYE	M TLRLMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV	
	JELVSKPYID	ITLNL MKTFG	VE..IAN.HH	YOQFVVKGGQ	OYHSPGRYL V	
	JELVSKPYID	ITLNL MKTFG	VE..IAN.HH	YOQFVVKGGQ	OYHSPGRYL V	
	JELVSKPYID	ITLNL MKTFG	VE..IAN.HH	YOQFVVKGGQ	OYHSPGRYL V	
	JELVSKPYID	ITLNL MKTFG	VE..IEN.QH	YOQFVVKGGQ	SYQSPGT YLV	
	JELVSKPYID	ITLHLMKTFG	VE..VEN.QA	YOQFIVRGNO	OYQSPGD YLV	
	JELVSKPYID	ITLHLMKAFG	VD..VVH.EN	YOIFHTKGGQ	TVBPCDTVIV	

[illegible]

3000	VIEPVMTRDH	TEKMLQGFCA	DI'IVETDKDG	VRHIRITGQ	KLVGQ.TIDV
	VIEPVMTRDH	TEKMLQGFCA	DLTVETDKDG	VRHIRITGQ	KLVGQ.TIDV
	VIEPIMTRDH	TEKMLQGFCA	NLTVEITDADG	VRTIRLEGRG	KLTGQ.VIDV
	VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGGQ	KLTA.A.DIFV
	IKELDVSRNH	TE'ETMFKH'FNI	PIEAEGLS..	..INTPEAI	RYIKPADFHV
	GKPIISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTTYIPKG	HYINPSEYVI
	GKPISQPYID	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNPAYEYVI
	DKLISVPYVE	MTLKLMEKFG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEKFG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEKFG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV
	DKLISVPYVE	MTLKLMEKFG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV
	DKLISVPYVE	MTLKLMEKFG	IS..VEHSSS	WDRFFVVRGGQ	KYKSPGKAFV
	DKLISIPYVE	MTLRLMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV
	DELVSKRPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKRPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKRPYID	ITLNLMTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DLVSKRPYID	ITLNLMTKTFG	VE..IEN.QH	YQQFVVKGGQ	SYQSPGYLV
	EIVSRPYID	ITLHLMKTFG	VE..VEN.QA	YQRFIVRGNO	QYQSPGDYLV
	EIVSKRPYID	ITLHLMKAFG	VD..VVH.EN	YQIFHIKGGQ	TYRSPGIYLV
	ELVSKRPYID	ITLAMMRDFG	VK..VEN.HH	YQKFQVKGNQ	SYISPKNYLV
	EIVSKRPYID	ITLKMQTFG	VE..VEN.OA	YQREIVRGNO	QYQSPGDYLV

[illegible]

300	VIEPVMTRDH	TEKMLQGFCA	DI'IVETDKDG	VRHIRITGQ	KLVGQ.TIDV
	VIEPVMTRDH	TEKMLQGFCA	DLTVETDKDG	VRHIRITGQ	KLVGQ.TIDV
	VIEPIMTRDH	TEKMLQGFCA	NLTVEITDADG	VRTIRLEGRG	KLTGQ.VIDV
	VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGQ	KLTA.A.DIFV
	IKELDVSRNH	<u>TE</u> TMFKHFNI	PIEAGLS..	..INTPEAI	RYIKPADFHV
	GKPISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTTYIPKG	HYINPSEYVI
	GKPISQPYID	MTTAMMRSG	ID..VQKSTT	EEHTYHIPQG	RYVNPAYEVI
	DKLISVPYVE	MTLKLMEKFG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEKFG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV
	DKLISVPYVE	MTLKLMEKFG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV
	DKLISVPYVE	MTLKLMEKFG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV
	DKLISVPYVE	MTLKLMEKFG	IS..VEHSSS	WDRFFVVRGGQ	KYKSPGKAFV
	DKLISIPYVE	MTLRLMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPGKAFV
	DELVSKPYID	ITLNLKMTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKPYID	ITLNLKMTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKPYID	ITLNLKMTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKPYID	ITLNLKMTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV
	DELVSKPYID	ITLNLKMTFG	VE..IEN.QH	YQQFVVKGGQ	SYQSPGTYYLV
	DELVSRPYID	ITLHLMKTFG	VE..VEN.QA	YQRFIVRGNQ	QYQSPGDYLV
	EI'LVSKPYID	ITLHLMKAFG	VD..VVH.EN	YQIFHIKGGQ	TYRSPGITYLV
	ELVSKPYID	ITLAMMRDFG	VK..VEN.HH	YQKFQVKGNQ	SYISPKNYLV
	EI'VSKPYID	ITLKMQTFG	VE..VEN.QA	YQRFVLVKGHQ	QYQSPHRELV
	ELVSKPYID	ITLHIMNSSG	VV..IEH.DN	YKLFYIKGNQ	SIVSPGDFLV
	ELVSKPYIE	ITLNLMARFG	VS..V.BRDG	WBAETIAPDA	WBAETIAPDA

300  
 VIEPVMTRDH TEKMLQGFCA DLTIVETDKDG VRHIRITGQ KLVGQ.TIDV  
 VIEPVMTRDH TEKMLQGFCA DLTIVETDKDG VRHIRITGQ KLVGQ.TIDV  
 VIEPIMTRDH TEKMLQGFCA NLTVETDADG VRTIRLEGRG KLTGQ.VIDV  
 VTEPHKSRDH TERMLSAFGV KLSGDQTS... ..VSIAGQ KLTA.A.DIFV  
 IKELDVSRNH TETMFKHFNI PIEAGLS... ..INTPEAI RYIKPADFHV  
 GKPI SKLYVD MTLKMEKFG IN.VET.STT EPTYTYIPKG HYINPSEYVI  
 GKPI SQPYID MTTAMMRSG ID..VQSTT EEHTYHIPQG RYVNPAYVI  
 DKLISVPYVE MTLKLMERFG VS..AEHSDS WDRFFVKGGQ KYKSPGNAYV  
 DKLISVPYVE MTLKLMERFG VS..VEHSDS WDRFFVKGGQ KYKSPGNAYV  
 DKLISVPYVE MTLKLMERFG VS..VEHTSS WDKFLVRGGQ KYKSPGKAYV  
 DKLISVPYVE MTLKLMERFG VF..VEHSSG WDRFLVKGGQ KYKSPGKAFV  
 DKLISVPYVE MTLKLMERFG IS..VEHSSS WDRFFVVRGGQ KYKSPGKAFV  
 DKLISIPIYVE MTLRLMERFG VK..AEHSDS WDRFYIKGGQ KYKSPKNAYV  
 BELVSKRPYID ITLNLMTKTFG VE..IAN.HH YQQFVVKGGQ QYHSPGRYLV  
 BELVSKRPYID ITLNLMTKTFG VE..IAN.HH YQQFVVKGGQ QYHSPGRYLV  
 BELVSKRPYID ITLNLMTKTFG VE..IAN.HH YQQFVVKGGQ QYHSPGRYLV  
 DLVSKRPYID ITLNLMTKTFG VE..IEN.QH YQQFVVKGGQ SYQSPGTYYLV  
 ELVSRPYID ITLHLMTKTFG VE..VEN.QA YQRFIVRGNO QYQSPGDYLV  
 ELVSKRPYID ITLHLMTKAFG VD..VVH.EN YQIFHIKGGQ TYRSPGIYYLV  
 ELVSKRPYID ITLAMMRDFG VK..VEN.HH YQKFQVKGNQ SYISPKNYYLV  
 ELVSKRPYID ITLKMOTFG VE..VEN.QA YQRFVLKGHQ QYQSPHRLV  
 ELVSKRPYID ITLHIMNSSG VV..IEH.DN YKLFYIKGNQ SIVSPGDFLV  
 ELISKPYIE ITLNLMARFG VS..V.RRDG WRAFTIARDA VYRGPGMAI

## Figure 20

[illegible]

	301		350
PG2982	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN
LBAA	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN
Agrobacterium CP4	PGDPSSTAFP	LVAALLVPGS	DVTILNVLMN
B. subtilis	PGDISSAAFF	LAAGAMVPNS	RIVLKNVGLN
S. aureus	PGDISSAAFF	IVAALITPGS	DVTIHNVGIN
S. cerevisiae	ESDASSATYP	LAFAA.MTGT	TVTVPNIGFE
A. nidulans	ESDASCATYP	LAVAA.VTGT	TCTVPNIGSA
B. napus	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT
A. thaliana	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT
N. tabacum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS
I. esculentum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTN
P. hybrida	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTT
Z. mays	EGDASSASYF	LAGAA.ITGG	TVTVEGCGTT
S. gallinarum	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK
S. typhimurium	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK
S. typhi	EGDASSASYF	LAAGG.IKGG	TVKVTGIGGK
E. coli	EGDASSASYF	LAAAA.IKGG	TVKVTGIGRN
K. pneumoniae	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRN
Y. enterocolitica	EGDASSASYF	LAAAA.IKGG	TVRVGTIGKQ
H. influenzae	EGDASSASYF	LAAGA.IK.G	KVKVTGIGKN
P. multocida	EGDASSASYF	LAAAA.IK.G	KVKVTGVGKN
A. salmonicida	EGDASSASYF	LAAGA.IK.G	KVRVTGIGKH
B. pertussis	EGDASTASYF	LALGA.IGGG	PVRVTGVGED
Consensus	D-S-----		
			-----MG----

Figure 20

	PG2982	351	400
	LBAA		
Agrobacterium CP4	EVLNARLAGG	EDVADLRVR.	ASKLKGVVVP
B. subtilis	EVINPRLAGG	EDVADLRVR.	ASKLKGVVVP
S. aureus	EIKPSADSGA	EPYGDLLIE.	TSSLKAVEIG
S. cerevisiae	QL.FNQTTGA	EPTASIRIQY	TPMLQIPITIE
A. nidulans	...TQTATS	TTVSGRPV..	...GTLKPLK
B. napus	...EQTETS	TTVTGPSD..	...GILRATS
A. thaliana	...SWTENS	VTVTGPSRDA	FGMRLHRAV.
N. tabacum	...SWTENS	VTVTGPPRDA	FGMRHLRAI.
I. esculentum	...TWTEENS	VTVKGPPRNS	SGMKHLRAV.
P. hybrida	...TWTEENS	VTVKGPPRNS	SGMKHLRAI.
Z. mays	...TWTETS	VTVTGPPREP	FGRKLHRAI.
S. gallinarum	...TWGDDF	I.....A	CTRGELHAI.
S. typhimurium	...TWGDDF	I.....A	CTRGELHAI.
S. typhi	...TWGDDF	I.....A	CTRGELHAI.
E. coli	...CWGDDY	I.....S	CTRGELNAI.
K. pneumoniae	...TWGEDY	I.....A	CTRGELNAI.
Y. enterocolitica	...SWGDDY	I.....E	CSRGELQGI.
H. influenzae	...TWGEDF	I.....Q	AEHAELNGI.
F. multocida	...TWGDDF	I.....Q	VEKGNLKI.
A. salmonicida	...TWGDDF	I.....E	AEQGPLHGV.
B. pertussis	...RYGPGW	IETRGVRAE	GGR..LKAF.
Consensus			

D-

Figure 20

	PG2982	401				450
	LBAA	AEG.....	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	DCTEGEMSLT
Agrobacterium CP4		AEG.....	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	DCTEGEMSLT
B. subtilis		AEG.....	ATVMNGLEEL	RVKESDRLSA	VANGLKINGV	DCDEGETSLV
S. aureus		AVG.....	TSTIKDAEEL	KVKETNRIDT	VVSELRLKGA	EIEPTADGMK
S. cerevisiae		SHSDSPNSAN	TTTIEGIANQ	RVKECNRIILA	MATELAKFGV	KTELPDGIQ
A. nidulans		IRPMEKSQTT	PPVSSGIANQ	RVKECNRIKA	MKDELAKFGV	ICREHDDGLE
B. napus		ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA	TV.EEGSDYC
A. thaliana		ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA	TV.EEGSDYC
N. tabacum		ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA	TV.VEGSDYC
L. esculentum		ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA	TV.VEGSDYC
P. hybrida		ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA	TV.EEGPDYC
Z. mays		ADG.....	PTAIRDVASW	RVKETERMIA	IRTELTKLGA	SV.EEGPDYC
S. gallinarum		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA	EV.EEGHDYI
S. typhimurium		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA	EV.EEGHDYI
S. typhi		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA	EV.EEGHDYI
E. coli		AKG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA	EV.EEGHDYI
K. pneumoniae		ARG.....	TTTLRNINYNW	RVKETDRLFA	MATELRKVGA	EV.EEGEDYI
Y. enterocolitica		ADG.....	PTVIRNINYNW	RVKETDRLSA	MATELRKVGA	EV.EEGQDYI
H. influenzae		SNG.....	ETVIRNINYNW	RVKETDRLTA	MATELRKVGA	EV.EEGEDFI
P. multocida		AEG.....	ETVIRNINYNW	RVKETDRLTA	MATELRKVGA	EV.EEGEDFI
A. salmonicida		I,PR.....	VPPHSQHLQL	AVRD.DRCTP	CTHGHRRÄQA	GVSEEGTTFI
B. pertussis		ADG.....	PCRLRNIGSW	RVKETDRIHA	MHTELEKLGA	GV.ÖSGADWL
Consensus			-V-----R-----			

Figure 20

	451		500
FG2982	VRGRPDGKGL G...GG....	TVATHLDHRI AMSFLVMGLA	.....A
LBAA	VRGRPDGKGL G...GG....	TVATHLDHRI AMSFLVMGLA	.....A
Agrobacterium CP4	VRGRPDGKGL GNASGA...	AVATHLDHRI AMSFLVMGLV	.....S
B. subtilis	VYGKQTLKG. ...GA...	AVSSHGDHRI GMLGIASCI	.....T
S. aureus	IHPSEFTN. ...AT...	DI. LTDHRI GMLAVACVL	.....S
S. cerevisiae	VHGLNSIKDL KVPSSSGPV	GVCTYDDHRV AMSFSLAGM	VNSQNERDEV
A. nidulans	IDGIDR.SNL RQPVG....	GVFCYDDHRV AFSFSL.SL	VTPQ.....
B. napus	VITP..PAKV KPA.....	EIDTYDDHRM AMAFSLAAC.	.....A
A. thaliana	VITP..PKKV KTA.....	EIDTYDDHRM AMAFSLAAC.	.....A
N. tabacum	IITP..PEKL NVT.....	EIDTYDDHRM AMAFSLAAC.	.....A
L. esculentum	IITP..PEKL NVT.....	EIDTYDDHRM AMAFSLAAC.	.....A
P. hybrida	IITP..PEKL NVT.....	DIDTYDDHRM AMAFSLAAC.	.....A
Z. mays	IITP..PEKL NVT.....	AIDTYDDHRM AMAFSLAAC.	.....A
S. gallinarum	RITP..PAKL QHA.....	DIGTYNDHRM AMCFSLVAL.	.....S
S. typhimurium	RITP..PAKL QHA.....	DIGTYNDHRM AMCFSLVAL.	.....S
S. typhi	RITP..PAKL QHA.....	DIGTYNDHRM AMCFSLVAL.	.....S
E. coli	RITP..PEKL NFA.....	EIATYNDHRM AMCFSLVAL.	.....S
K. pneumoniae	RITP..PLTL QFA.....	EIGTYNDHRM AMCFSLVAL.	.....S
Y. enterocolitica	RVVP..PAQL IAA.....	EIGTYNDHRM AMCFSLVAL.	.....S
H. influenzae	RIQPLALNQF KHA.....	NIETYNDRM AMCFSLIAL.	.....S
P. multocida	RIQPLNLAQF QHA.....	ELNI. HDHRM AMCFALIAL.	.....S
A. salmonicida	TRDADADPAQA RRD.....	R. HLQRSRI AMCFSLVAL.	.....S
B. pertussis	EVAPPEPGGW RDA.....	HIGTWDHRM AMCFLLAAF.	.....G
Consensus	-----	-----R-----	-----

Figure 20

	501		538
PG2982	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI
LBAA	EKPVTVDDSN	MIATSFPEFM	ELSIL...
Agrobacterium CP4	ENPVTVDDAT	MIATSFPEFM	ELSIL...
B. subtilis	EEPIEIEHTD	AIHVSYPTFF	DI.MAGLGAKI
S. aureus	SEPVKIKQFD	AVNVSEFPGFL	EHLNKLKSKS
S. cerevisiae	ANPVRILERH	CTGKTWPGWW	PKLKLQNEG
A. nidulans	. PTLILEKE	CVGKTWPGWW	DVLH.....
B. napus	DVPVTIKDPG	CTRKTFPDYF	DTLRQLFKV.
A. thaliana	DVPITINDSG	CTRKTFPDYF	QVLESITKH.
N. tabacum	DVPVTIKDPG	CTRKTFPNYF	QVLERITKH.
I. esculentum	DVPVTIKNPG	CTRKTFPDYF	DVLQQYSKH.
P. hybrida	DVPVTINDPG	CTRKTFPNYF	EVLQKYSKH.
Z. mays	EVPTVTRDPG	CTRKTFPDYF	DVLQQYSKH.
S. gallinarum	DTPVTILDPK	CTAKTFPDYF	DVLSTFVKH.
S. typhimurium	DTPVTILDPK	CTAKTFPDYF	EQLARMSTPA
S. typhi	DTPVTILDPK	CTAKTFPDYF	EQLARMSTPA
E. coli	DTPVTILDPK	CTAKTFPDYF	EQLARMSTPA
K. pneumoniae	DTPVTILDPK	CTAKTFPDYF	EQLARISQAA
Y. enterocolitica	DTPVTILDPK	CTAKTFPDYF	EQLARISQAA
H. influenzae	NTPVITILDPK	CTAKTFPTFF	EQLARISQIA
P. multocida	KTSVTILDPG	CTAKTFPTFL	NEFE...KI
A. salmonicida	DIAVTINDPG	CTSKTFPDYF	ILFTLNTREV
B. pertussis	IAAVRILDPG	CVSKTFPDYF	DKLASVSQAV
Consensus	-----P-----		DVYAGLLAAR

Figure 20

004434039.127599

ACGGGCTTGT	ACGGTAGTAG	GGGTCCCGAG	CACAAAGCG	GTGCCGGCAA	GCAGACTAA	60
TTTCCATGCG	GAAATAATGCT	ATTTCATTGG	TTTGCCCTCT	GGTCTGGCAA	TGTTGCTAG	120
GCGATCGCCCT	GTGGAATTTA	ACAAACTGTC	GCCCTTCCAC	TGACCATGGT	AACGATGTTT	180
TTTACTTTCCCT	TGACTAACCG	AGGAAATTTT	GGCGGGGGC	AGAAATGCCA	ATACAATTTA	240
GGTTGGTCTT	CCCCTGCCCT	AATTTGTCCC	CTCC	ATG	GCC	292
				Met	Ala	
				Leu	Leu	
				Ser	Leu	
AAC	AAT	CAT	CAA	TCC	CAT	340
Asn	Asn	His	Gln	Ser	His	
				Gln	Arg	
				Leu	Thr	
				Val	Asn	
				Pro	Pro	
				Ala	Gln	
GGG	GTC	GCT	TTG	ACT	GGC	388
Gly	Val	Ala	Leu	Thr	Gly	
				Arg	Leu	
				Val	Pro	
				Gly	Asp	
				Lys	Ser	
				Ile		
TCC	CAT	CGG	GCC	TTG	ATG	436
Ser	His	Arg	Ala	Leu	Met	
				Leu	Gly	
				Ala	Ile	
				Ala	Thr	
				Gly	Glu	
				Thr	Ile	
ATC	GAA	GGG	CTA	CTG	TTG	484
Ile	Glu	Gly	Leu	Leu	Gly	
				Glu	Asp	
				Pro	Arg	
				Ser	Thr	
				Ala	His	
				Cys		

Figure 21

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TCA GCC CAG GTA AAG ACC TGC CTG TTG CTA GCG GGG TTA ACC ACC GAG	868
Ser Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu	
185	190
GGG GAC ACC ACG GTT ACA GAA CCA GCT CTA TCC CGG GAT CAT AGC GAA	916
Gly Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu	
200	205
CCC ATG TTG CAG GCC TTT GGA GCC AAA TTA ACC ATT GAT CCA GTA ACC	964
Arg Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Thr Ile Asp Pro Val Thr	
215	220
CAT AGC GTC ACT GTC CAT GGC CCG GCC CAT TTA ACG GGG CAA CGG GTG	1012
His Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val	
235	240
GTG GTG CCA GGG GAC ATC AGC TCG GCG GCC TTT TGG TTA GTG GCG GCA	1060
Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala	
250	255
TCC ATT TTG CCT GGA TCA GAA TTG TTG GTG GAA AAT GTA GGC ATT AAC	1108
Ser Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn	
265	270
CCC ACC AGG ACA GGG GTG TTG GAA GTG TTG GCC CAG ATG GGG GCG GAC	1156
Pro Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp	
280	285
	290

# Figure 21

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00464064-111599

ATP ACC CCG GAG AAT GAA CGA TTG GTA ACC GCG GAA CCG GTA GCA GAT	1204
Ile Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp	
295	300
CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA	1252
Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu	
315	320
ATP CCC CGA CTT ATP GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG	1300
Ile Ile. Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala	
330	335
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG	1348
Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg	
345	350
GTT AAA GAA AGC GAT CCG CTG GCG GCC ATT GCT TCG GAG TTG GGC AAA	1396
Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys	
360	365
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTT GAA ATT CAA GCG	1444
Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly	
375	380
UGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC	1492
Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Ser Leu Thr Asp His Arg	
395	400
	405

## Figure 21

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004099-121599

ATG GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGG GGG CAA ACA 1540  
 Ile Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gly Gln Thr  
 410 415 420

ATT ATT AAC CGG GCG GAA GCG GCC GCC ATT TCC TAT CCA GAA TTT TTT 1588  
 Ile Ile Asn Arg Ala Gln Ala Ala Ala Ile Ser Tyr Pro Gln Phe Phe  
 425 430 435

GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG 1635  
 Gly Thr Leu Gly Gln Val Ala Gln Gly  
 440 445

GCGCGTTTGT AAATGTTTTA CCAAGTACT TTGGGTAA GCGCCACGCA AGTCTGCCA 1695

GGGTAATTTA TCCGCAATTTG ACCAATCGGC ATGACCGTA TCGTTCAAC TGGTAATTG 1755

TCCCTTTAAT TCCTTAAAG CTCGCTTAA ACTGCCCAAC GTATCTCCGT AATGGCGAGT 1815

GAGTAAAGAT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAGCCT GCATCACTGA 1875

CCACTTATTA CTTTCCGGA 1894

TTTAAAAACCA ATGAGTAAAA AAATTATTTT TCTGGCACAC GCGCTTTT TTGCATTTT	60
CCCCCATTTT TCCCGCACCA TAACGTTGGT TTTATAAAG GAAATG ATG ATG ACC	115
Met Met Thr	
1	
AAATATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACC	163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr	
5 10 15	
ATA TGC GGC GAT AAA TCA ATG TCG CAT GCG GCC TTA TTA TTA GCA GCG	211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala	
20 25 30 35	
TAA GCA GAA GGA CAA ACC GAA ATC CGC GGC TTT TTA GCG TGC GCG GAT	259
Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp	
40 45 50	
TGT TTG GCG ACC GCG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA	307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln	
55 60 65	
AGA GAA AAA GAA ATA GTG ACC ATT CGC GGT GTG GGA TTT CTG GGT TTG	355
Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu	
70 75 80	

## Figure 22

SHEET 1 of 5

09461099 121599

CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG 403  
 Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met 85 90 95

CGT TTA TTG GCA GGA ATT TTG GCA GCG CAG CGC TTT GAG AGC GTG TTA 451  
 Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu 100 105 110 115

TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT ACG 499  
 Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr 120 125 130

CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT ACG 547  
 Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr 135 140 145

GCG CCG TTA CAT ATT TCA GGA CGC CCG CTG ACC GGC ATT GAT TAC GCG 595  
 Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala 150 155 160

TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA 643  
 Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly 165 170 175

TTA TTG GCT GAC GGT ACC ACG CGG CTG CAT ACT TGC GGC ATC AGT CGC 691  
 Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg 180 185 190 195

09464099 121699

GAC CAC ACC GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC 739  
 Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile 210  
 200

AAG AAA GAG CAA ATG ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC 787  
 Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys 225  
 215 220

GTC CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT 835  
 Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe Phe Met Val 240  
 230 235

GCG GCT TTG ATT GCG CCG CCG GCG GAA GTC GTT ATT CGT AAT GTC GGC 883  
 Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg Asn Val Gly 255  
 245 250

ATT AAT CCG ACC GCG GCG GCA ATC ATT ACT TTG TTG CAA AAA ATG GGC 931  
 Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly 275  
 260 265 270

GGA CCG ATT GAA TTG CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG 979  
 Gly Arg Ile Glu, Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val 290  
 280 285

GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CCG GGC ATT ACG GTG GCG 1027  
 Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala 305  
 295 300

## Figure 22

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49464039-121699

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT 1075  
 Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile  
 310 315 320

GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA 1123  
 Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu  
 325 330 335

TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA 1171  
 Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Glu Asn Leu  
 340 345 350 355

CAA ACT TTG GGC GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA 1219  
 Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile  
 360 365 370

TAT GGA AGA AGC GAT CCG CAA TTT TTA CCG GCG CCG GTG AAC AGT TTT 1267  
 Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe  
 375 380 385

GGC GAT CAT CCG ATT CCG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG 1315  
 Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala  
 390 395 400

GCA GGT GAA TTA TTG ATT GAT GAC GCG GCG GTG GCG GCG GTT TCT ATG 1363  
 Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met  
 405 410 415

## Figure 22

SHEET 4 of 5

05454099-1234567

UCC CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GCA GAA	1411
Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn Val Gly Glu	
420 425 430 435	

AAA GAT GCG AAA AAT TGT CAC GAT TGATGCTCCT AGCGGTGTG GAAAGGCAC	1465
Lys Asp Ala Lys Asn Cys His Asp	
440	

GTTGGCCCAA GCTT	1479
-----------------	------

0946406621699





	121		160
PG2982	TY.DMKTSEI	GDASLSKRPM	GRVLNPLREM
LBAA	TY.DMKTSEI	GDASLSKRPM	GRVLNPLREM
Agrobacterium CP4	VY.DFDSTFI	GDASLTKRPM	GRVLNPLREM
Synechocystis sp. PCC6803	GQKDCLEFVT	GDDSLRHRPM	SRVIOPLQOM
B. subtilis	G.RPFYSAVA	GDESIKRPM	KRVTEPLKKM
D. nodosus	AQR.FESVLC	GDESLEKRPM	QRIITPLVQM
S. aureus	GLGN.ESVLS	GDVSIKRRPM	DRVLRPLKM
Consensus	GD-S--RPM	-RV--PL--M	----I-----
	161		200
PG2982	RMPLTLIGPK	TANPITYRVP	MASAQVKSAY
LBAA	RMPLTLIGPK	TANPITYRVP	MASAQVKSAY
Agrobacterium CP4	RLPVTLRGPK	TPTPITYRVP	MASAQVKSAY
Synechocystis sp. PCC6803	KFAPLAVQGS	QLKPIHYHSP	IASAQVKSCL
B. subtilis	EFTPLSVSGA	SLKGIDYVSP	VASAQIKSAV
D. nodosus	T.APLHISGR	PLTGIDYALP	LPSAQLKSCL
S. aureus	.YTPLIIKPS	VIKGINYQME	VASAQVKSAY
Consensus	----I-Y----	--SAQ-KS--	-LA-L-----
	201		240
PG2982	TTVIEPVMTR	DHTEKMLQGF	.....GADLT
LBAA	TTVIEPVMTR	DHTEKMLQGF	.....GADLT
Agrobacterium CP4	TTVIEPIPTR	DHTEKMLQGF	.....GANLT
Synechocystis sp. PCC6803	TTVTEPALSR	DHSERMLQAF	.....GAKLT
B. subtilis	TTVTEPHKSR	DHTEKMLSAF	.....GVKLS
D. nodosus	TRLHTCGISR	DHTEKMLPLF	.....GALE
S. aureus	TIKELDVS	NHTEKMFHF	NIPAEGLS
Consensus	T-----R-H-E-ML--F	-----L--	-----V--

Figure 23





669727-65049460

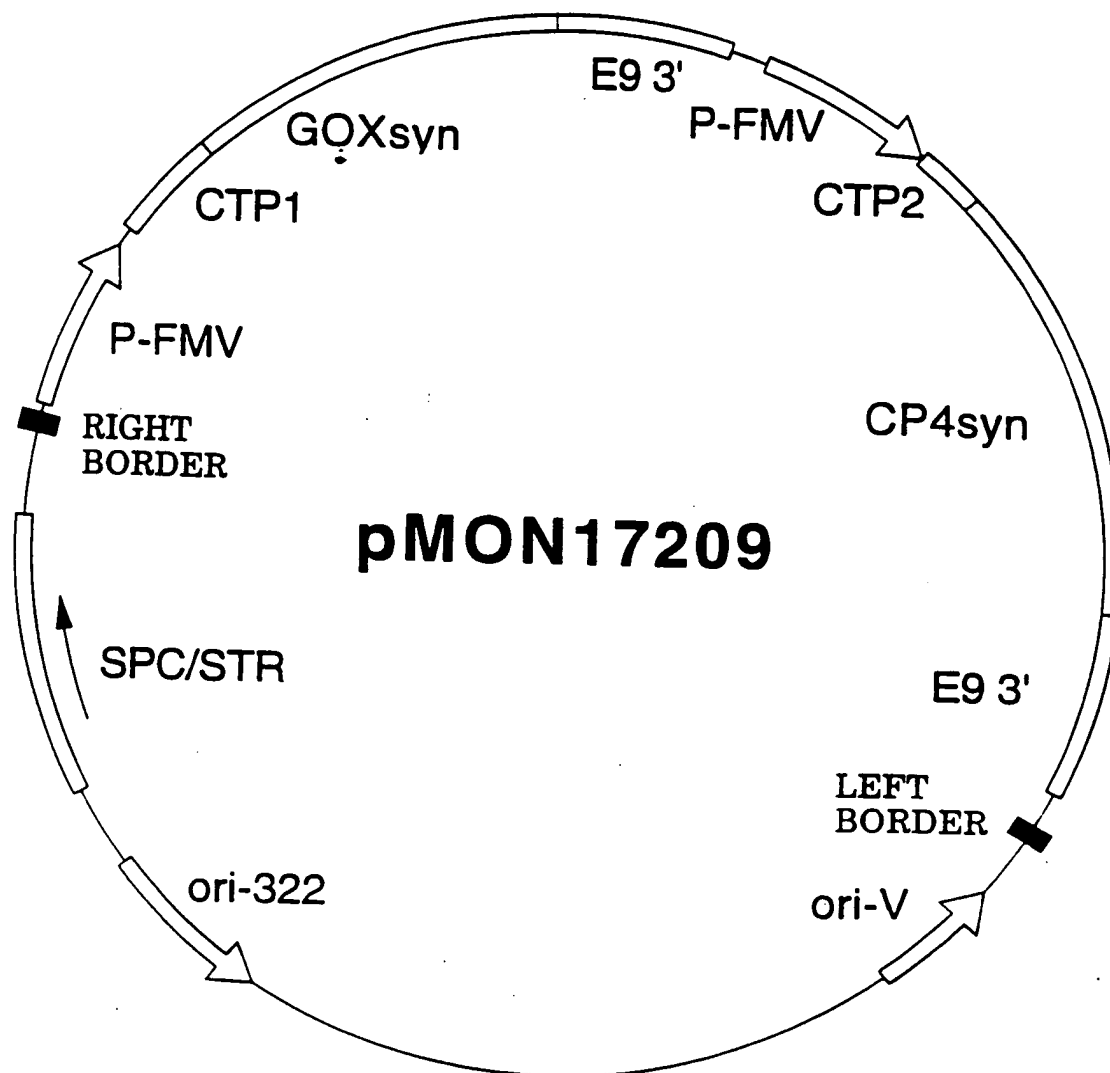
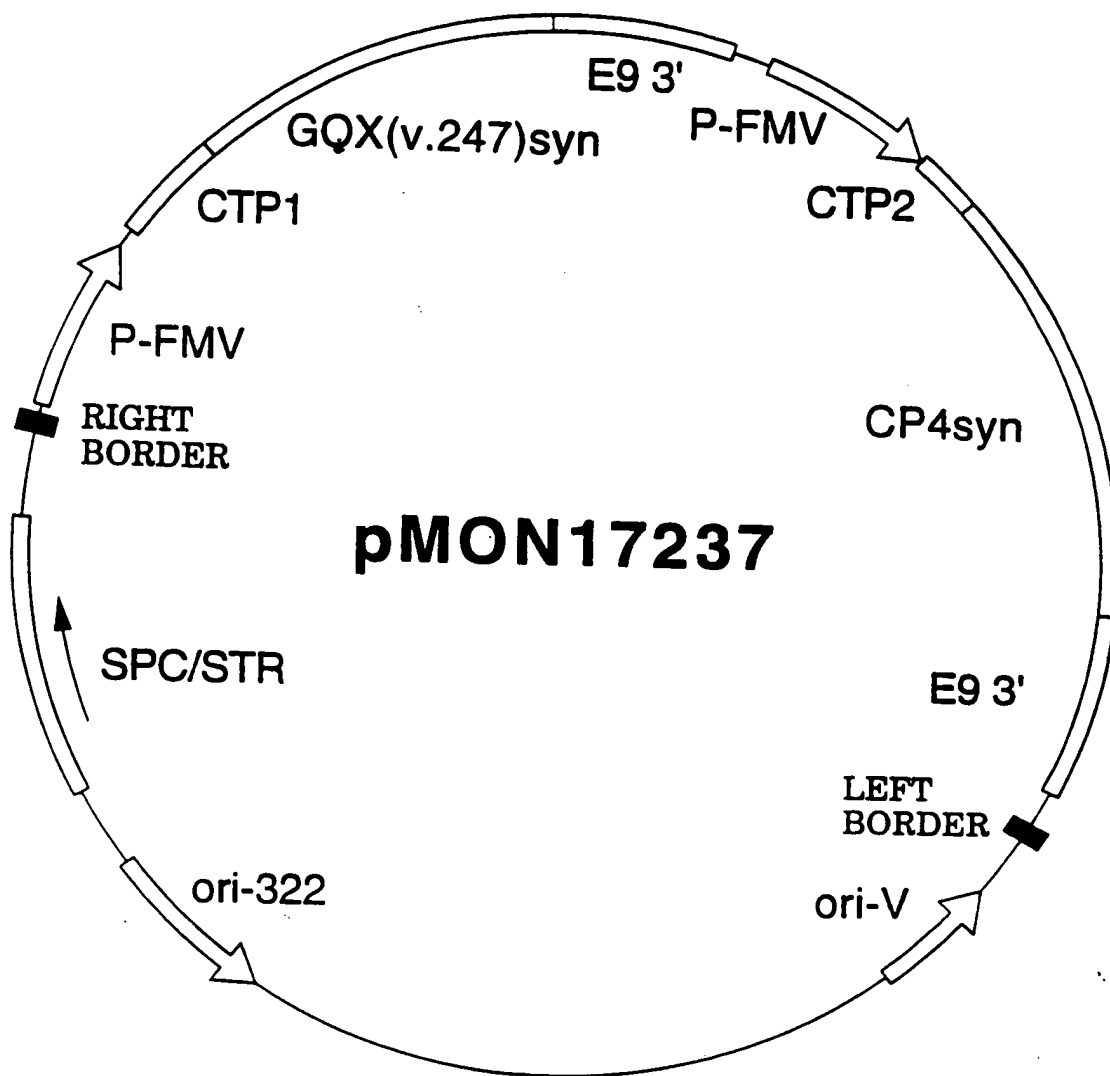


Figure 24



**Figure 25**